SEQUENCE LISTING

<110> Goedegebuur, Frits
      Gualfetti, Peter
      Mitchinson, Colin
      Neefe, Paulien

<120> Novel CBH1 Homologs and Variant CBH1
  Cellulases

<130> GC793-3

<140> US 10/804,785
<141> 2004-03-19

<150> US 60/456,368
<151> 2003-03-21

<150> US 60/458,696
<151> 3003-03-27

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1491
<212> DNA
<213> Hyprocrea jecorina

<400> 1
cagtcggcct gcactctcca atcggagact cacccgcctc tgacatggca gaaatgctcg   60
tctggtggca cttgcactca acagacaggc tccgtggtca tcgacgccaa ctggcgctgg   120
actcacgcta cgaacagcag cacgaactgc tacgatggca acacttggag ctcgacccta   180
tgtcctgaca acgagacctg cgcgaagaac tgctgtctgg acggtgccgc ctacgcgtcc   240
acgtacggag ttaccacgag cggtaacagc ctctccattg gctttgtcac ccagtctgcg   300
cagaagaacg ttggcgctcg cctttacctt atggcagcg acacgaccta ccaggaattc   360
accctgcttg gcaacgagtt ctctttcgat gttgatgttt cgcagctgcc gtgcggcttg   420
aacggagctc tctacttcgt gtccatggac gcggatggtg gcgtgagcaa gtatcccacc   480
aacaccgctg cgccaagta cggcacgggg tactgtgaca gccagtgtcc ccgcgatctg   540
aagttcatca atggccaggc caacgttgag ggctgggagc cgtcatccaa caacgcgaac   600
acgggcattg gaggacacgg aagctgctgc tctgagatgg atatctggga ggccaactcc   660
atctccgagg ctcttacccc ccacccttgc acgactgtcg gccaggagat ctgcgagggt   720
gatgggtgcg gcggaactta ctccgataac agatatggcg gcacttgcga tcccgatggc   780
tgcgactgga acccataccg cctgggcaac accagcttct acggccctgg ctcaagcttt   840
accctcgata ccaccaagaa attgaccgtt gtcacccagt cgagacgtc gggtgccatc   900
aaccgatact atgtccagaa tggcgtcact ttccagcagc ccaacgccga gcttggtagt   960
tactctggca acgagctcaa cgatgattac tgcacagctg aggaggcaga attcggcgga   1020
tcctcttttct cagacaaggg cggcctgact cagttcaaga aggctacctc tggcggcatg   1080
gttctggtca tgagtctgtg ggatgattac tacgccaaca tgctgtggct ggactccacc   1140
tacccgacaa acgagacctc ctccacaccc ggtgccgtgc gcggaagctg ctccaccagc   1200
tccggtgtcc ctgctcaggt cgaatctcag tctcccaacg ccaaggtcac cttctccaac   1260
atcaagttcg gacccattgg cagcaccggc aaccctagcg cggcaaccc tcccggcgga   1320
aacccgcctg gcaccaccac cacccgccgc ccagccacta ccactggaag ctctcccgga   1380
cctacccagt ctcactacgg ccagtgcggc ggtattggct acagcggccc cacggtctgc   1440
gccagcggca caacttgcca ggtcctgaac ccttactact ctcagtgcct g   1491

<210> 2
<211> 497
<212> PRT
<213> Hyprocrea jecorina

1

<400> 2

```
Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1               5                   10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
            85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
    115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
            195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
            245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
            275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340                 345                 350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
            355                 360                 365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
            405                 410                 415
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
            420                 425                 430
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
            435                 440                 445
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser
    450                 455                 460
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
465                 470                 475                 480
```

2

```
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                485                 490                 495
Leu


<210> 3
<211> 1635
<212> DNA
<213> Hyprocrea orientalis

<400> 3
cgtcatctcg gccttcttgg ccacggcccg tgctcagtcg gcctgcactc tccaaacgga      60
gactcacccg tctctgacat ggcagaaatg ctcgtctggc ggcacttgca cccagcagac     120
aggctccgtg gtcatcgacg ccaactggcg ctggactcac gcgactaaca gcagcacgaa     180
ctgctacgac ggcaacactt ggagctcaac cctatgccct gacaacgaga cttgcgcgaa     240
gaattgctgc ctggacggtg ccgcctatgc gtccacgtac ggagtcacca cgagtgccga     300
cagcctctcc atcggcttcg tcacgcaatc tgcacagaag aacgttggcg cccgtctcta     360
cctgatggcg agtgacacga cttaccagga gttcacgctg cttggcaacg agttctcttt     420
tgacgttgat gtttcgcagc tgccgtaagt gacaaccatt ccccgcgagg ccatcttctc     480
attggttccg agctgacccg ccgatctaag atgtggcttg aacggcgctc tgtacttcgt     540
gtctatggat gcggatggtg gcgtgagcaa gtatcccacc aacaccgccg gcgccaagta     600
cggcacgggc tactgcgaca gccagtgccc ccgcgatctc aagttcatca acggccaggc     660
caacgttgaa ggctgggagc cgtcctccaa caacgccaac acgggtattg gcggacacgg     720
aagctgctgc tctgagatgg atatctggga ggccaactcc atctccgagg ctctgactcc     780
tcacccttgc acgactgttg gccaggagat ctgcgacggt gacggctgcg gcggaaccta     840
ctccaacgac cgatatggtg gtacttgcga tcctgatggt tgtgattgga atccataccg     900
cttgggcaac accagcttct atggccctgg ctcgagcttc accctcgata ccaccaagaa     960
gttgaccgtt gtcacccagt tcgagacctc gggtgccatc aaccgttact atgtccagaa    1020
cggcgtcact taccagcaac ccaacgccga gctcggtagt tactctggta atgagctcaa    1080
cgatgactac tgcacagctg aggagtcgga attcggcggc tcctccttct cggacaaggg    1140
cggccttact cagttcaaga aggccacttc cggcggcatg gtcctggtca tgagcttgtg    1200
ggatgacgtg agttgataga cagcattcac attgtcgttg aaagacgggc ggctaaccg     1260
agacatatga tatctaacag tactacgcca acatgctgtg gctggactcc acctacccga    1320
caaacgagac ctcctccacc cccggcgccg tgcgcggaag ctgctccacc agctccggcg    1380
tccccgctca gctcgagtcc cagtccccca cgccaaggt cgtctactcc aacatcaagt     1440
tcgggcccat tggcagcacc ggcaacccca gcggcggaaa ccctcctggc ggaaaccctc    1500
ccggcaccac caccacccgc cgcccagcta ccaccactgg aagctctccc ggacctactc    1560
agactcacta cggccagtgc ggcggcatcg gctacagcgg ccctacggtc tgcgccagcg    1620
gcacgacctg ccagg                                                    1635

<210> 4
<211> 17
<212> PRT
<213> Hyprocrea orientalis

<400> 4
Met Tyr Arg Lys Leu Ala Val Ile Ser Ala Phe Leu Ala Thr Ala Arg
 1               5                   10                  15
Ala


<210> 5
<211> 497
<212> PRT
<213> Hyprocrea orientalis

<400> 5
Gln Ser Ala Cys Thr Leu Gln Thr Glu Thr His Pro Ser Leu Thr Trp
 1               5                   10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
                20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
```

3

```
            35                        40                        45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                        55                        60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                        70                        75                        80
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser Leu Ser Ile Gly Phe Val
                85                        90                        95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
                100                       105                       110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
                115                       120                       125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                       135                       140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                       150                       155                       160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                       170                       175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
                180                       185                       190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
                195                       200                       205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                       215                       220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Asp Gly
225                       230                       235                       240
Asp Gly Cys Gly Gly Thr Tyr Ser Asn Asp Arg Tyr Gly Gly Thr Cys
                245                       250                       255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
                260                       265                       270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
                275                       280                       285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
                290                       295                       300
Val Gln Asn Gly Val Thr Tyr Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                       310                       315                       320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ser
                325                       330                       335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
                340                       345                       350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
                355                       360                       365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                       375                       380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                       390                       395                       400
Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Pro Asn Ala Lys Val
                405                       410                       415
Val Tyr Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
                420                       425                       430
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
                435                       440                       445
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Thr
    450                       455                       460
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
465                       470                       475                       480
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                485                       490                       495
Leu
```

<210> 6
<211> 1589

4

```
<212> DNA
<213> Hyprocrea schweintzii

<400> 6
tcggcctgca ctctccaaac ggagactcac ccgtctctga catggcagaa atgctcgtct      60
ggcggcactt gcacccagca gacaggctcc gtggtcatcg acgccaactg gcgctggact     120
cacgctacta acagcagcac gaactgctac gacggcaaca cttggagctc aaccctgtgc     180
cctgacaatg agacttgcgc gaagaactgc tgcctggacg gtgccgccta tgcgtccacg     240
tacggagtca ccacgagtgc cgacagcctc tccatcggct tcgtgacaca gtctgcacag     300
aaaaacgttg gcgcccgtct ctacctgatg gcgagtgaca cgacttacca ggagttcacg     360
ctgcttggca acgagttctc attcgacgtt gatgtttcgc agctgccgta agtgacaacc     420
attcccccga cgccatcttc tcattggttc gaagctgacc cgccgatcta agatgtggct     480
tgaacggcgc tctttacttc gtgtccatgg acgcagatgg tggcgtgagc aagtatccca     540
ccaacaccgc cggcgccaag tacggcacgg ctactgtga cagccagtgc cccgcgatc      600
tcaagtttat caacggccag gccaacgttg aaggctggga ccgtcctcc aacaacgcca     660
acacgggtat tggcggacac ggaagctgct gctccgagat ggatatctgg gaggccaact     720
ccatctccga ggctcttact cctcacccctt gcacgaatgt tggccaggag atctgcgacg    780
gtgacggctg cggcggaacc tactccaacg accgatatgg tggtacttgc gatcctgatg    840
gttgtgattg gaatccatac cgcttgggca acaccagctt ctatggccct ggctcgagct    900
tcaccctcga taccaccaag aagttgaccg tcgtcaccca gttcgagact tcgggtgcca    960
tcaaccgtta ctatgtccag aatggcgtca cttaccagca acccaacgcc gagctcggca   1020
gttactctgg taatgagctc aacgatgcct actgcacagc tgaagagtcg gaatttggcg   1080
gttcctcctt ctcggacaag ggcggcctta ctcagttcaa gaaggccact tccggcggca   1140
tggtcctggt catgagcttg tgggatgacg tgagtccata gaacagcatt cacattgtcg   1200
tcggaaagac ggccggctaa ccgagacatt acagtactac gccaacatgc tgtggctgga   1260
ctccacctac ccgacaaacg agacctcctc accccccggt gccgtgcgcg gaagctgctc   1320
caccagctcc ggcgtcccag ctcagctcga gtcccagtcc gccaacgcca aggtcgtcta   1380
ctccaacatc aagttcggac ccattggcag caccggcaac cccagcggcg aaaccctcc    1440
tggcggaaac cctcccggca ccaccaccac ccgccgccca gctaccacca ctggaagctc   1500
tcccggacct actcagactc actatggcca gtgcggcggc atcggctaca gcggccctac   1560
gatctgcgcc agcggcacga cctgccagg                                     1589

<210> 7
<211> 17
<212> PRT
<213> Hyprocrea schweintzii

<400> 7
Met Tyr Arg Lys Leu Ala Val Ile Thr Ala Phe Leu Ala Thr Ala Arg
 1               5                  10                  15
Ala


<210> 8
<211> 497
<212> PRT
<213> Hyprocrea schweintzii

<400> 8
Gln Ser Ala Cys Thr Leu Gln Thr Glu Thr His Pro Ser Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
                20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
```

5

```
                  100                      105                      110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
          115                      120                      125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
          130                      135                      140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                      150                      155                      160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                  165                      170                      175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
              180                      185                      190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
          195                      200                      205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
      210                      215                      220
Leu Thr Pro His Pro Cys Thr Asn Val Gly Gln Glu Ile Cys Asp Gly
225                      230                      235                      240
Asp Gly Cys Gly Gly Thr Tyr Ser Asn Asp Arg Tyr Gly Gly Thr Cys
                  245                      250                      255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
              260                      265                      270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
          275                      280                      285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
      290                      295                      300
Val Gln Asn Gly Val Thr Tyr Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                      310                      315                      320
Tyr Ser Gly Asn Glu Leu Asn Asp Ala Tyr Cys Thr Ala Glu Glu Ser
                  325                      330                      335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
              340                      345                      350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
          355                      360                      365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
      370                      375                      380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                      390                      395                      400
Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Ala Asn Ala Lys Val
                  405                      410                      415
Val Tyr Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
              420                      425                      430
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
          435                      440                      445
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Thr
      450                      455                      460
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Ile Cys
465                      470                      475                      480
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                  485                      490                      495
Leu
```

<210> 9
<211> 1588
<212> DNA
<213> Trichoderma konilangbra

<400> 9
```
tcggcctgca ccattcaagc ggagactcac ccgcctctga catggcagaa atgctcatcc      60
ggtggtagtt gcacctcgca aaccggttct gtggtgattg acgcgaactg gcgatggact     120
cacgcgacta acagcaccac gaactgctac gacggtaaca cttggagctc cagtctttgc     180
cccgacaatg agagttgcgc aaagaactgc tgcctggacg gtgcagccta cgcatccacg     240
```

6

```
tacggagtca ccacgagtgc tgatagcctc tccattggct tcgtcactca gtctcagcag    300
aagaatgttg gcgctcgtct ctacctgatg gcaagcgaca cgacctacca ggaatttacc    360
ctgcttggca acgagttctc tttcgatgtt gatgtttcac agctgccgta agtgactagc    420
atttacctcc gacgccatct cattgattcc cagctgacgg ccaattcaag atgtggcttg    480
aacggagccc tttacttcgt gtccatggac gcggatggtg gcgtgagcaa gtatccctcc    540
aacactgccg gcgccaagta cggcacgggc tactgcgata gccagtgtcc ccgtgatttg    600
aagttcatca cggcgaggc caacgttgag ggctgggagc cggcttcgaa caacgccaac    660
acgggtattg gcggacacgg aagctgctgc tctgagatgg atatctggga ggccaactcc    720
atctctgagg cccttactcc tcaccccttgc acgactgtcg gccaggccat ttgcgatggt    780
gacggctgcg gtggaaccta ctccgatgac cgatatggtg gtacttgcga tcctgatggc    840
tgtgactgga acccataccg cttgggcaac accagcttct acggcccccgg ctcgagcttc    900
accctcgaca ccaccaagaa gatgaccgtc gtcacccagt tcgctacttc gggtgccatc    960
aaccgatact atgtccagaa tggcgtcact ttccagcagc ccaacgccga gctcggtagc    1020
tactctggca acacgctcaa cgatgcttac tgcgcagctg aagaggcgga attcggcgga    1080
tcatctttct cagacaaggg tggccttacc caattcaagc aggctacttc aggcggcatg    1140
gtcttggtta tgagcctgtg ggatgacgtg agttcatgga tagcattgac attgtcgaga    1200
gaaccatagc cgctgaccga gacacaacag tactacgcca acatgctgtg gctggactcc    1260
atctacccga cgaacgagac ctcctctacc cccggtgccg cgcgcggaag ctgctctacc    1320
agctccggtg tccctgccca gctcgagtct cagtctacca cgccaaggt cgtcttctcc    1380
aacatcaagt tcggacccat tggcagcact ggtaactcca gcggcggaaa accccccgggc    1440
ggaggaaacc ccccgggcac caccaccacc cgacgcccag ctaccaccac cggaagctct    1500
cccggaccta ctcagacaca ctatggccag tgcggtggaa ttgggtactc gggccccacg    1560
gtctgcgcca gcggcagcac atgccagg                                       1588
```

<210> 10
<211> 17
<212> PRT
<213> Trichoderma konilangbra

<400> 10
```
Met Tyr Arg Lys Leu Ala Val Ile Thr Ala Phe Leu Ala Thr Ala Arg
 1               5                  10                  15
Ala
```


<210> 11
<211> 498
<212> PRT
<213> Trichoderma konilangbra

<220>
<221> VARIANT
<222> 273
<223> Xaa = Any Amino Acid

<400> 11
```
Gln Ser Ala Cys Thr Ile Gln Ala Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Ser Cys Thr Ser Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Thr Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Ser Leu Cys Pro Asp Asn
    50                  55                  60
Glu Ser Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Gln Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
```

7

```
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                     135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Ser
145                     150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ala Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Ala Ile Cys Asp Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asp Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Xaa Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Met
        275                 280                 285
Thr Val Val Thr Gln Phe Ala Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Thr Leu Asn Asp Ala Tyr Cys Ala Ala Glu Glu Ala
                325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
                340                 345                 350
Lys Gln Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
        355                 360                 365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Ile Tyr Pro Thr Asn
    370                 375                 380
Glu Thr Ser Ser Thr Pro Gly Ala Ala Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400
Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Thr Asn Ala Lys Val
                405                 410                 415
Val Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Ser
                420                 425                 430
Ser Gly Gly Asn Pro Pro Gly Gly Gly Asn Pro Pro Gly Thr Thr Thr
        435                 440                 445
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
    450                 455                 460
Thr His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465                 470                 475                 480
Cys Ala Ser Gly Ser Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
                485                 490                 495
Cys Leu


<210> 12
<211> 1592
<212> DNA
<213> Trichoderma pseudokoningii

<400> 12
tcggcctgca ccctccagac ggaaactcac ccgcctctga catggcagaa atgctcatct      60
ggtggcactt gcacccaaca gacgggctcc gtggtcatcg acgcgaactg gcgctggact     120
cacgctacga acagcagcac gaactgctac gacggtaaca cttggagctc aaccttgtgc     180
cctgacaatg agacttgcgc gaagaactgc tgcttggatg gtgccgccta cgcgtcgacg     240
tacggagtca ccacgagcgc tgacagcctc tccattggct cgtcactca gtctgcgcag      300
aagaatgtcg cgcccgtctc tacttgatg gcgagtgaca cgacctacca agaatttacc      360
ctgcttggca acgagttctc cttcgatgtt gatgtttccc agctgccgta agtggccaac     420
```

8

```
tacacccctt gacggtatcc tctcattggt tcccagctga ctcgcgaaat taagatgtgg    480
cttgaacgga gctctttact tcgtgtccat ggacgcggat ggtggcgtga gcaagtatcc    540
cacaaacact gccggcgcca agtacggcac gggttactgt gacagccagt gccctcgtga    600
tctcaagttc atcaacggcg aggccaacgt tgagggctgg gagccgttct ccaacaacgc    660
caacacgggc attggcggac atggaagctg ctgctctgag atggatatct gggaggccaa    720
ctccatctct gaggctctta ctcctcatcc ttgcacgacc gtcgggcagg aaatttgcga    780
tggtgactcc tgcggcggaa cctactccgg tgatcgatat ggcggtactt gcgatcctga    840
tggctgcgat tggaacccat accgcttggg caacaccagc ttctacgggc ccggctcaag    900
cttcgctctt gataccacca agaagttgac cgttgtcacc cagttcgaga cttcgggcgc    960
tatcaaccgg tactacgtcc agaatggcgt cactttccag cagcccaacg ccgagctcgg   1020
tagttactct ggcaactcgc tcgacgatga ctactgcgcg gctgaagagg cggagtttgg   1080
tggctcttct ttctcggaca agggcggcct tactcaattc aaaaaggcta cttccggtgg   1140
catggtcttg gtcatgagct tgtgggatga tgtgagttca tgaatagcat tcaaacagtc   1200
aacagaataa cagcagctga ctgagacaca atagtactac gccaacatgc tgtggctgga   1260
ctccacctac ccgacgaacg agacctcttc caccccrggt gccgtgcgcg gaagctgctc   1320
caccagctcc ggtgtccctg ctcagcttga gtcccagtct tccaacgcca aggtcgtata   1380
ctccaacatc aagttcggcc ctatcggcag caccggcaac tccagcggcg gtagccctcc   1440
cggcggagga aaccctcccg gtaccacgac caccacgccg ccagctacct ccactggaag   1500
ctctcccggc cctactcaga cgcactatgg ccagtgcggt ggtattgggt actcgggccc   1560
cacggtctgc gcgagtggca gcacttgcca gg                                  1592


<210> 13
<211> 17
<212> PRT
<213> Trichoderma pseudokoningii


<400> 13
Met Tyr Arg Lys Leu Ala Val Ile Thr Ala Phe Leu Ala Thr Ala Arg
 1               5                  10                  15
Ala



<210> 14
<211> 498
<212> PRT
<213> Trichoderma pseudokoningii


<400> 14
Gln Ser Ala Cys Thr Leu Gln Thr Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
                20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
            35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
        50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Val Glu Gly Trp
            180                 185                 190
```

9

```
Glu Pro Phe Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
    195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210             215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Asp Gly
225                 230                 235                 240
Asp Ser Cys Gly Gly Thr Tyr Ser Gly Asp Arg Tyr Gly Gly Thr Cys
            245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Ala Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Ser Leu Asp Asp Asp Tyr Cys Ala Ala Glu Glu Ala
            325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340                 345                 350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
        355                 360                 365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400
Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Ser Asn Ala Lys Val
            405                 410                 415
Val Tyr Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Ser
            420                 425                 430
Ser Gly Gly Ser Pro Pro Gly Gly Gly Asn Pro Pro Gly Thr Thr Thr
        435                 440                 445
Thr Arg Arg Pro Ala Thr Ser Thr Gly Ser Ser Pro Gly Pro Thr Gln
    450                 455                 460
Thr His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465                 470                 475                 480
Cys Ala Ser Gly Ser Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
            485                 490                 495
Cys Leu


<210> 15
<211> 497
<212> PRT
<213> Trichoderma reesei

<400> 15
Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
  1             5                 10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
            85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
```
10

```
              115                  120                  125
    Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
         130                  135                  140
    Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
    145                  150                  155                  160
    Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                  165                  170                  175
    Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
                  180                  185                  190
    Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
                  195                  200                  205
    Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
         210                  215                  220
    Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
    225                  230                  235                  240
    Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                  245                  250                  255
    Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
                  260                  265                  270
    Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
                  275                  280                  285
    Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
         290                  295                  300
    Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
    305                  310                  315                  320
    Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                  325                  330                  335
    Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
                  340                  345                  350
    Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
                  355                  360                  365
    Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
         370                  375                  380
    Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
    385                  390                  395                  400
    Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                  405                  410                  415
    Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
                  420                  425                  430
    Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
                  435                  440                  445
    Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser
         450                  455                  460
    His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
    465                  470                  475                  480
    Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                  485                  490                  495
    Leu


    <210> 16
    <211> 495
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> consensus sequence

    <400> 16
    Gln Ser Ala Cys Thr Leu Gln Thr Glu Thr His Pro Pro Leu Thr Trp
    1                  5                  10                  15
    Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
```

11

```
              20                      25                      30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                      40                      45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                      55                      60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                      70                      75                      80
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser Leu Ser Ile Gly Phe Val
                85                      90                      95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                     105                     110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
            115                     120                     125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                     135                     140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                     150                     155                     160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                     170                     175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                     185                     190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
            195                     200                     205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                     215                     220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Asp Gly
225                     230                     235                     240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Arg Tyr Gly Gly Thr Cys Asp
                245                     250                     255
Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe
                260                     265                     270
Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr
            275                     280                     285
Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val
            290                     295                     300
Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr
305                     310                     315                     320
Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu
                325                     330                     335
Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys
            340                     345                     350
Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp Asp
            355                     360                     365
Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu
    370                     375                     380
Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser Ser
385                     390                     395                     400
Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Asn Ala Lys Val Val Tyr
                405                     410                     415
Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly
            420                     425                     430
Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg
            435                     440                     445
Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Thr His Tyr
            450                     455                     460
Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser
465                     470                     475                     480
Gly Thr Thr Cys Gln Val Leu Asn Glu Tyr Tyr Ser Gln Cys Leu
                485                     490                     495
```

<210> 17
<211> 19

12

```
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
atgtatcgga agttggccg                                              19

<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
ttacaggcac tgagagtag                                              19
```